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SEQUENCE LISTING TECH CENTER 1600/2900 MAR 21 2002

<110> Lechler, Robert I.  
Dorling, Anthony

<120> IMMUNOSUPPRESSION BY BLOCKING T CELL CO-STIMULATION SIGNAL 2 (B7/CD28 INTERACTION)

<130> 2292/0H795

<140> US 09/674,462

<141> 2001-05-08

<150> PCT/ GB99/01350

<151> 1999-04-30

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 223

<212> PRT

<213> Sus scrofa

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro  
20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
115 120 125

Cys	Lys	Val	Glu	Leu	Leu	Tyr	Pro	Pro	Pro	Tyr	Tyr	Val	Gly	Met	Gly
130							135					140			
Asn	Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser
145							150				155			160	
Asp	Phe	Leu	Leu	Trp	Ile	Leu	Ala	Ala	Val	Ser	Ser	Gly	Leu	Phe	Phe
							165				170			175	
Tyr	Ser	Phe	Leu	Ile	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys
							180				185			190	
Arg	Ser	Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu
							195				200			205	
Pro	Glu	Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn	
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 <213> Sus scrofa

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 gcccaacctg cagtagtgc gccaacacgc cgggtgttg ccagcttgc gtgtgagttat 180  
 gggctgcag gcaaagctgc cgaggtccgg gtgacagtgc tgccgcggc cggcagccag 240  
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 atcacagctg tttcttgag caaaatgcta aagaaaagaa gtcctttac tacaggggtc 600  
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 cccatcaatt ga 672

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 <211> 400  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> pCTLA4-Ig construct (Figure 4)

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro  
 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala  
 35 40 45

Asn Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ala Gly  
 50 55 60

Lys Ala Ala Glu Val Arg Val Thr Val Leu Arg Arg Ala Gly Ser Gln  
 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Thr  
 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Thr Glu Asn Lys Val  
 100 105 110

Asn Leu Thr Ile Gln Gly Leu Arg Ala Val Asp Thr Gly Leu Tyr Ile  
 115 120 125

Cys Lys Val Glu Leu Leu Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly  
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160

Asp Gly Gly Ser Gly Gly Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr  
 165 170 175

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
 180 185 190

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
 195 200 205

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
 210 215 220

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 225 230 235 240

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
 245 250 255

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 260 265 270

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 275 280 285

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 290 295 300

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 305 310 315 320

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 325 330 335

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 340 345 350

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 355 360 365

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 370 375 380

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 385 390 395 400

<210> 4  
 <211> 722  
 <212> DNA  
 <213> Phage library

<400> 4

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 ctccagggaa ggggctggag tgggtcttag ctattcgtgg tagtggtggt agcacatact 180  
 acgcagactc cgtgaaggc cggttacca tctccagaga caattccaag aacacgctgt 240  
 atctgcaaat gaacagcctg agagccgagg acacggccgt gtattactgt gcaagagctg 300  
 gtcgtatTTT gtttactat tggggccaag gtaccctggt caccgtctcg agtggtgag 360  
 gcggttcagg cggaggtggc tctggcggtt gtgcacttca gtctgtctg actcagccac 420  
 cctcagcgtc tgggaccccc gggcagcggg tcaccatctc ttgttctgga agcagctcca 480  
 acatcggaaag taattatgtt tactggtacc agcagctccc aggaacggcc cccaaactcc 540  
 tcatctatag gaataatcag cggccctcag gggccctga ccgattctct ggctccaagt 600  
 ctggcacctc agcctccctg gccatcagtg ggctccggtc cgaggatgag gctgattatt 660  
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 gt 722

<210> 5  
 <211> 240  
 <212> PRT  
 <213> Phage library

&lt;400&gt; 5

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20 25 30Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95Ala Arg Ala Gly Arg Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
115 120 125Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly  
130 135 140Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn  
145 150 155 160Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
165 170 175Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro  
180 185 190Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile  
195 200 205Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp  
210 215 220Asp Asp Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
225 230 235 240

<210> 6  
 <211> 729  
 <212> DNA  
 <213> Phage library

<400> 6

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ccaggctcca gggaaaggggc tggagtgggt ctcagctatt agtggtagtg gtggtagcac 180
atactacgca gactccgtga agggccgggtt caccatctcc agagacaatt ccaagaacac 240
gctgtatctg caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcaag 300
agctggtcgt atttgtttg actattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
tggaggcggt tcaggcggag gtggctctgg cggtagtgca cttcagtgctg tgctgactca 420
gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttgtt ctggaaagcag 480
ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
actcctcatc tataggaata atcagcggcc ctcaggggtc cctgaccgat tctctggctc 600
caagtctggc acctcagcct ccctggccat cagtgggtc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct ggtattcggc ggagggacca agctgaccgt 720
ccttaggtgc 729
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<210> 7  
 <211> 738  
 <212> DNA  
 <213> Phage library

<400> 7

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ccggcagccc ccaggaaagg gactggagt gattgggtat atctattaca gtgggagcac 180
caactacaac ccctccctca agagtcgagt caccatatac tagacacgt ccaagaacca 240
gttctccctg aagctgagct ctgtgaccgc tgccggacacg gccgtgtatt actgtgcaag 300
aatgcggaaag gataagttt gactattgggg ccaaggtacc ctggtcaccg tctcgagtgg 360
tggaggcggt tcaggcggag gtggctctgg cggtagtgca cttcagtgctg tgctgactca 420
gccaccctca gcgtctggga cccccgggca gagggtcacc atctcttgtt ctggaaagcag 480
ctccaacatc ggaagtaatt atgtatactg gtaccagcag ctcccaggaa cggcccccaa 540
actcctcatc tataggaata atcagcggcc ctcaggggtc cctgaccgat tctctggctc 600
caagtctggc acctcagcct ccctggccat cagtgggtc cggtccgagg atgaggctga 660
ttattactgt gcagcatggg atgacagcct gtttgttattc ggcggaggga ccaagctgac 720
cgtcctaggt gcggccgc 738
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<210> 8  
 <211> 739  
 <212> DNA  
 <213> Phage library

<400> 8

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aaggtttcct gcaaggcatt tggatacacc ttcaccagct actatatgca ctgggtgcga 120
caggccctg gacaagggtc tgagtggatg ggaataatca accctagtg ggtagcaca 180
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caagctacgc acagaagttc cagggcagag tcaccatgac cagggacacg tccacgagca 240  
 cagtctacat ggagctgagc agcctgagat ctgaggacac ggcctgtat tactgtcaa 300  
 gaatggctcc ctatgtaat acgcttggtt tttggggcca aggtaccctg gtcaccgtct 360  
 cgagtggtgg aggccgttca ggcggaggtg gctctggcgg tagtgactt cagtctgtgc 420  
 tgactcagga ccctgctgtg tctgtggcct tggacagac agtcaggatc acatgccaag 480  
 taggagacag cctcagaagc tattatgcaa gctggatcca gcagaagcca ggacaggccc 540  
 ctgtacttgt catctatggt aaaaacaacc gcccctcagg gatcccagac cgattctctg 600  
 gctccagctc aggaaacaca gtttccttga ccatcactgg ggctcaggcg gaagatgagg 660  
 ctgactatta ctgtaactcc cggacagca gtggtttac tgtattcggc ggagggacca 720  
 agctgaccgt cctaggtgc 739

<210> 9  
 <211> 729  
 <212> DNA  
 <213> Phage library

<400> 9  
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 tgaagatctc ctgtaaagggt tctggataca gctttaccag ctactggatc ggctgggtgc 120  
 gccagatgcc cgggaaaggc ctggagtgga tggggatcat ctatcctggt gactctgata 180  
 ccagatacag cccgtccttc caaggccagg tcaccatctc agccgacaag tccatcagca 240  
 cgcctaccc gcagtggagc agcctgaagg cctcggacac ggcctgtat tactgtcaa 300  
 gatttcgct tggtggttt gactattggg gccaaggatc cctggtcacc gtctcgagtg 360  
 gtggaggcgg ttcaggcgg a ggtggctctg gcggtagtgc acttgacatc cagttgaccc 420  
 agtctccatg ttcctgtctg catctgttagg agacagatc accatcaactt gccggggccag 480  
 tcagggcatt agcagttatt tagcctggta tcagaaaaa ccagggaaag cccctaagct 540  
 cctggcttat gctgcatcca cttgcaaaag tggggtccca tcaaggttca gcggcagtgg 600  
 atctgggaca gaattcactc tcacaatcag cagcctgcag cctgaagatt ttgcaactta 660  
 ttactgtcaa cagcttaata gttaccgctt gacgttcggc caagggacca agctggaaat 720  
 caaacgtgc 729

<210> 10  
 <211> 240  
 <212> PRT  
 <213> Phage library

<400> 10  
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 20 25 30  
  
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
  
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65	70	75	80
Leu Gln Met Asn Ser	Leu Arg Ala Glu Asp	Thr Ala Val Tyr Tyr	Cys
85	90	95	
Ala Arg Ala Gly Arg Ile	Leu Phe Asp Tyr Trp	Gly Gln Gly	Thr Leu
100	105	110	
Val Thr Val Ser Ser Gly	Gly Gly Ser Gly	Gly Gly Ser Gly	
115	120	125	
Gly Ser Ala Leu Gln Ser	Val Leu Thr Gln Pro	Pro Ser Ala Ser Gly	
130	135	140	
Thr Pro Gly Gln Arg Val	Thr Ile Ser Cys	Ser Gly Ser Ser Ser	Asn
145	150	155	160
Ile Gly Ser Asn Tyr Val	Tyr Trp Tyr Gln Gln	Leu Pro Gly Thr Ala	
165	170	175	
Pro Lys Leu Leu Ile Tyr	Arg Asn Asn Gln Arg	Pro Ser Gly Val Pro	
180	185	190	
Asp Arg Phe Ser Gly Ser	Lys Ser Gly Thr Ser Ala	Ser Leu Ala Ile	
195	200	205	
Ser Gly Leu Arg Ser Glu	Asp Glu Ala Ser Tyr	Tyr Cys Ala Ala Trp	
210	215	220	
Asp Asp Ser Leu Val Phe	Gly Gly Thr Lys	Leu Thr Val Leu Gly	
225	230	235	240

<210> 11  
 <211> 246  
 <212> PRT  
 <213> Phage library

<400> 11			
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Ser Glu Thr Leu Ser	Leu Thr Cys Thr Val	Ser Gly Gly Ser Val	Ser
20	25	30	
Ser Gly Ser Tyr Tyr	Trp Ser Trp Ile Arg	Gln Pro Pro Gly Lys Gly	
35	40	45	

Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn  
 50 55 60

Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn  
 65 70 75 80

Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 85 90 95

Tyr Tyr Cys Ala Arg Met Arg Lys Asp Lys Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly  
 115 120 125

Gly Ser Gly Gly Ser Ala Leu Gln Ser Val Leu Thr Gln Pro Pro Ser  
 130 135 140

Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser  
 145 150 155 160

Ser Ser Asn Ile Gly Ser Asn Tyr Val Tyr Trp Tyr Gln Gln Leu Pro  
 165 170 175

Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asn Asn Gln Arg Pro Ser  
 180 185 190

Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser  
 195 200 205

Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Val  
 210 215 220

Ala Ala Trp Asp Asp Ser Leu Phe Val Phe Gly Gly Thr Lys Leu  
 225 230 235 240

Thr Val Leu Gly Ala Ala  
 245

<210> 12  
 <211> 242  
 <212> PRT  
 <213> Phage library

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 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Léu Glu Trp Met  
                  35                         40                         45  
 Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe  
                  50                         55                         60  
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr  
                  65                         70                         75                         80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                  85                         90                         95  
 Ala Arg Val Ala Pro Tyr Val Asn Thr Leu Val Phe Trp Gly Gln Gly  
                  100                         105                         110  
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly  
                  115                         120                         125  
 Ser Gly Gly Ser Ala Leu Ser Ser Glu Leu Thr Gln Asp Pro Ala Val  
                  130                         135                         140  
 Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser  
                  145                         150                         155                         160  
 Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
                  165                         170                         175  
 Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro  
                  180                         185                         190  
 Asp Arg Phe Ser Gly Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile  
                  195                         200                         205  
 Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg  
                  210                         215                         220  
 Asp Ser Ser Gly Phe Thr Val Phe Gly Gly Thr Lys Leu Thr Val  
                  225                         230                         235                         240  
 Leu Gly

<210> 13  
 <211> 240  
 <212> PRT  
 <213> Phage library

&lt;400&gt; 13

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20 25 30Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
35 40 45Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
50 55 60Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
65 70 75 80Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Val Tyr Tyr Cys  
85 90 95Ala Arg Phe Ser Leu Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu  
100 105 110Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
115 120 125Gly Ser Ala Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser  
130 135 140Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
145 150 155 160Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
165 170 175Lys Leu Leu Val Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser  
180 185 190Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser  
195 200 205Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Asn  
210 215 220Ser Tyr Arg Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
225 230 235 240

<210> 14  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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 cctggccctg cactctcctg tttttcttc tcttcatccc tgtcttctgc aaagcaatgc 180  
 acgtggccca gcctgctgtg gtactggcca gcagccgagg catgccagc tttgtgtgtg 240  
 agtatgcatttccat tccaggcaaa gccactgagg tccgggtgac agtgcattcg 300  
 gcccagggtgac tgaagtctgt gccggcaacct acatgatggg gaatgagttg accttcctag 360  
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 tgagggccat ggacacggga ctctacatct gcaaggtgga gctcatgtac ccaccggcat 480  
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 attctgactt ctttcctctgg atccattgcag cagttagttc ggggttgttt ttttatact 600  
 ttcttcctcac agctgtttct ttgagcaaaa tgctaaagaa aagaagccct cttacaacag 660  
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<210> 15  
 <211> 223  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala  
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 Thr Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro  
 20 25 30  
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala  
 35 40 45  
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
 50 55 60  
 Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
 65 70 75 80  
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr  
 85 90 95  
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
 100 105 110  
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly  
 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
 165 170 175

Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn  
 210 215 220

<210> 16  
 <211> 773  
 <212> DNA  
 <213> Homo sapiens

<400> 16

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 ctggatcgga cctggAACCT gggcgagaca gtggagctga agtgcaggt gctgctgtcc 180  
 aaccccacgt cgggctgctc gtggctcttc cagccgcgcg gcccgcgcg cagtcccacc 240  
 ttcctccat acctctccca aaacaagccc aaggcggccg aggggcttga caccctagg 300  
 ttctcgggca agaggttggg ggacaccttc gtcctcaccc tgagcgactt cgcggagag 360  
 aacgagggtct actatttctg ctcggccctg agcaactcca tcattactt cagccacttc 420  
 gtgccggtct tcctgccagc gaagcccacc acgacgcccag cggccgcgacc accaaccac 480  
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